

Figure 1

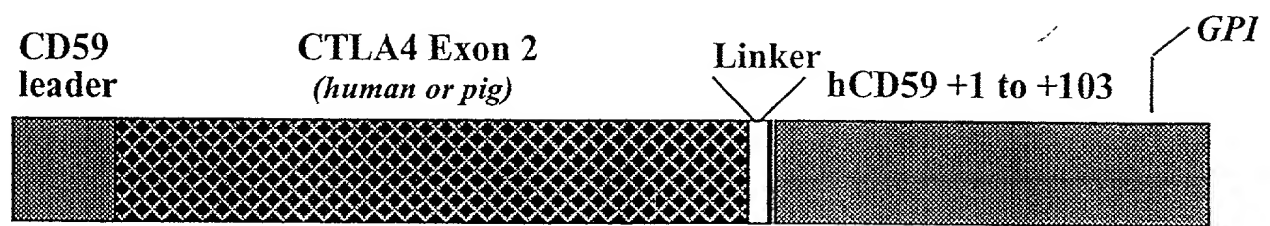


Diagram of Chimeric Molecule

Fig 1

Sequence Range: 1 to 833

```

      10      20      30      40      50
GGATCCTGGGCGCCGCCAGGTTCTGTGGACAATCACAATGGGAATCCAAG
CCTAGGACCCGCGGCGGTCCAAGACACCTGTTAGTGTACCTTAGGTTC
                                M G I Q>
                                >
                                M G I Q>
                                >

      60      70      80      90     100
GAGGGTCTGTCCTGTTCTGGGCTGCTGCTCGTCCTAGCTGTCTTCTGCCAT
CTCCCAGACAGGACAAGCCCGACGACGAGCAGGATCGACAGAAGACGGTA
G G S V L F G L L L V L A V F C H>
      TRANSLATION OF PIGCCBAM/RIMP [ A] >
G G S V L F G L L L V L A V F C H>
      >

     110     120     130     140     150
TCAGGTCATAGCCTGCATATGCACGTGGCCCAGCCTGCAGTGGTGCTGGC
AGTCCAGTATCGGACGTATACGTGCACCGGGTCGGACGTCACCACGACCG
S G H S L H M H V A Q P A V V L A>
      TRANSLATION OF PIGCCBAM/RIMP [ A] >
S G H S L H M H V A Q P A V V L A>
      >

     160     170     180     190     200
CAACAGCCGGGGTGTTGCCAGCTTTGTGTGTGAGTATGGGTCTGCAGGCA
GTTGTCGGCCCCACAACGGTCGAAACACACACTCATACCAGACGTCCGT
N S R G V A S F V C E Y G S A G>
      TRANSLATION OF PIGCCBAM/RIMP [ A] >
N S R G V A S F V C E Y G S A G>
      >

     210     220     230     240     250
AAGCTGCCGAGGTCCGGGTGACAGTGCTGCGGCGGGCCGGCAGCCAGATG
TTCGACGGCTCCAGGCCCACTGTCACGACGCCGCGCCGGCTCGGTCTAC
K A A E V R V T V L R R A G S Q M>
      TRANSLATION OF PIGCCBAM/RIMP [ A] >
K A A E V R V T V L R R A G S Q M>
      >

     260     270     280     290     300
ACTGAAGTCTGTGCCGCGACATATACTGTGGAGGATGAGTTGACCTTCCT
TGACTTCAGACACGGCGCTGTATATGACACCTCCTACTCAACTGGAAGGA
T E V C A A T Y T V E D E L T F L>
      TRANSLATION OF PIGCCBAM/RIMP [ A] >

```

Fig. 2A1

T E V C A A T Y T V E D E L T F L>
>

310 320 330 340 350
TGATGACTCTACATGCACTGGCACCTCCACCGAAAACAAAGTGAACCTCA
ACTACTGAGATGTACGTGACCGTGGAGGTGGCTTTTGTTCCTTCACTTGGAGT
D D S T C T G T S T E N K V N L>
TRANSLATION OF PIGCCBAM/RIMP [A]>
D D S T C T G T S T E N K V N L>
>

360 370 380 390 400
CCATCCAAGGGCTGAGAGCCGTGGACACTGGGCTCTACATCTGCAAGGTG
GGTAGGTTCCCGACTCTCGGCACCTGTGACCCGAGATGTAGACGTTCCAC
T I Q G L R A V D T G L Y I C K V>
TRANSLATION OF PIGCCBAM/RIMP [A]>
T I Q G L R A V D T G L Y I C K V>
>

410 420 430 440 450
GAGCTCCTGTACCCACCACCCTACTATGTGGGTATGGGCAACGGGACCCA
CTCGAGGACATGGGTGGTGGGATGATACCCCATACCCGTTGCCCTGGGT
E L L Y P P P Y Y V G M G N G T Q>
TRANSLATION OF PIGCCBAM/RIMP [A]>
E L L Y P P P Y Y V G M G N G T Q>
>

460 470 480 490 500
GATTTATGTCATTGATCCAGAACCATGCCCAGATTCTGATTTCCGGTGGCG
CTAAATACAGTAACTAGGTCTTGGTACGGGTCTAAGACTAAAGCCACCGC
I Y V I D P E P C P D S D F G G>
TRANSLATION OF PIGCCBAM/RIMP [A]>
I Y V I D P E P C P D S D F G G>
>

510 520 530 540 550
GTGGCGGTGGCATGCAGTGCTACAACTGTCCTAACCCAACTGCTGACTGC
CACCGCCACCGTACGTCACGATGTTGACAGGATTGGGTTGACGACTGACG
G G G G M Q C Y N C P N P T A D C>
TRANSLATION OF PIGCCBAM/RIMP [A]>
G G G G M Q C Y N C P N P T A D C>
>

560 570 580 590 600
AAAACAGCCGTCAATTGTTTCATCTGATTTTGATGCGTGTCTCATTACCAA
TTTTGTGCGGCAGTTAACAAGTAGACTAAACTACGCACAGAGTAATGGTT
K T A V N C S S D F D A C L I T K>

TRANSLATION OF PIGCCBAM/RIMP [A] >
K T A V N C S S D F D A C L I T K>
>

610 620 630 640 650
AGCTGGGTTACAAGTGTATAACAAGTGTGGAAGTTTGAGCATTGCAATT
TCGACCCAATGTTTCACATATTGTTTACAACCTTCAAACCTCGTAACGTTAA
A G L Q V Y N K C W K F E H C N>

TRANSLATION OF PIGCCBAM/RIMP [A] >
A G L Q V Y N K C W K F E H C N>
>

660 670 680 690 700
TCAACGACGTCAACAACCCGCTTGAGGGAAAATGAGCTAACGTACTACTGC
AGTTGCTGCAGTGTGGGCGAACTCCCTTTTACTCGATTGCATGATGACG
F N D V T T R L R E N E L T Y Y C>

TRANSLATION OF PIGCCBAM/RIMP [A] >
F N D V T T R L R E N E L T Y Y C>
>

710 720 730 740 750
TGCAAGAAGGACCTGTGTAACTTTAACGAACAGCTTGAAAATGGTGGGAC
ACGTTCTTCCTGGACACATTGAAATTGCTTGTCGAACCTTTTACCACCCTG
C K K D L C N F N E Q L E N G G T>

TRANSLATION OF PIGCCBAM/RIMP [A] >
C K K D L C N F N E Q L E N G G T>
>

760 770 780 790 800
ATCCTTATCAGAGAAAACAGTTCTTCTGCTGGTGACTCCATTTCTGGCAG
TAGGAATAGTCTCTTTTGTCAAGAAGACGACCACTGAGGTAAAGACCGTC
S L S E K T V L L L V T P F L A>

TRANSLATION OF PIGCCBAM/RIMP [A] >
S L S E K T V L L L V T P F L A>
>

810 820 830
CAGCCTGGAGCCTTCATCCCTAAGTCGGAATTC
GTCGGACCTCGGAAGTAGGGATTACAGCCTTAAG
A A W S L H P *>

TRANSLATION OF P >
A A W S L H P *>
>

Sequence Range: 1 to 262

```
      10      20      30      40      50
MGIQGGSVLFGLLLVLAVFCHSGHSLHMHVAQPAVVLANSRGVASFVCEY

      60      70      80      90     100
GSAGKAAEVRVTVLRRAGSQMTEVCAATYTVEDELTFLLDDSTCTGTSTEN

     110     120     130     140     150
KVNLTIQGLRAVDGTGLYICKVELLYPPPYVGMNGTQIYVIDPEPCTDS

     160     170     180     190     200
DFGGGGGGMQCYNCPNPTADCKTAVNCSSDFDAKLITKAGLQVYNKCWKF

     210     220     230     240     250
EHCNFNDVTTTRLRENELTYCYCKKDLNCFNEQLENGGTSLSSEKTVLLLVT

     260
PFLAAAWSLHP*
```

Fig 2A2

Sequence Range: 1 to 830

10 20 30 40 50
GGATCCTGGGCGCCGCAGGTTCTGTGGACAATCACAATGGGAATCCAAGG
CCTAGGACCCGCGGCGTCCAAGACACCTGTTAGTGTTACCCTTAGGTTCC
M G I Q G>

60 70 80 90 100
AGGGTCTGTCTTCTCGGGCTGCTGCTCGTCCTGGCTGTCTTCTGCCATT
TCCCAGACAGGACAAGCCCGACGACGAGCAGGACCGACAGAAGACGGTAA
G S V L F G L L L V L A V F C H>
TRANSLATION OF HUCCBAM/RIMP [A]>

110 120 130 140 150
CAGGTCATAGCCTGCAGATGCACGTGGCCCAGCCTGCTGTGGTACTGGCC
GTCCAGTATCGGACGTCTACGTGCACCGGGTCGGACGACACCATGACCGG
S G H S L Q M H V A Q P A V V L A>
TRANSLATION OF HUCCBAM/RIMP [A]>

160 170 180 190 200
AGCAGCCGAGGCATCGCCAGCTTTGTGTGTGAGTATGCATCTCCAGGCAA
TCGTCCGGCTCCGTAGCGGTCGAAACACACACTCATACTAGAGGTCCGTT
S S R G I A S F V C E Y A S P G K>
TRANSLATION OF HUCCBAM/RIMP [A]>

210 220 230 240 250
AGCCACTGAGGTCCGGGTGACAGTGCTTCGGCAGGCTGACAGCCAGGTGA
TCGGTGACTCCAGGCCCACTGTCACGAAGCCGTCCGACTGTCGGTCCACT
A T E V R V T V L R Q A D S Q V>
TRANSLATION OF HUCCBAM/RIMP [A]>

260 270 280 290 300
CTGAAGTCTGTGCGGCAACCTACATGACGGGGAATGAGTTGACCTTCCTA
GACTTCAGACACGCCGTTGGATGTACTGCCCTTACTCAACTGGAAGGAT
T E V C A A T Y M T G N E L T F L>
TRANSLATION OF HUCCBAM/RIMP [A]>

310 320 330 340 350
GATGATTCCATCTGCACGGGCACCTCCAGTGGAAATCAAGTGAACCTCAC
CTACTAAGGTAGACGTGCCCCGTGGAGGTCACCTTTAGTTCACTTGGAGTG
D D S I C T G T S S G N Q V N L T>
TRANSLATION OF HUCCBAM/RIMP [A]>

360 370 380 390 400
TATCCAAGGACTGAGGGCCATGGACACGGGACTCTACATCTGCAAGGTGG
ATAGGTTCTGACTCCCGGTACCTGTGCCCTGAGATGTAGACGTTCCACC

Fig 2B1

I Q G L R A M D T G L Y I C K V>

TRANSLATION OF HUCCBAM/RIMP [A] >

410 420 430 440 450
AGCTCATGTACCCACCGCCATACTACCTGGGCATAGGCAACGGAACCCAG
TCGAGTACATGGGTGGCGGTATGATGGACCCGTATCCGTTGCCTTGGGTC
E L M Y P P P Y Y L G I G N G T Q>

TRANSLATION OF HUCCBAM/RIMP [A] >

460 470 480 490 500
ATTTATGTAATTGATCCAGAACCGTGCCAGATTCTGACGCCTCCGCCTC
TAAATACATTAAGTCTTGGCACGGGTCTAAGACTGCGGAGGCGGAG
I Y V I D P E P C P D S D A S A S>

TRANSLATION OF HUCCBAM/RIMP [A] >

510 520 530 540 550
CGCCTCCCTGCAGTGCTACAACCTGTCCTAACCCAACTGCTGACTGCAAAA
GCGGAGGGACGTCACGATGTTGACAGGATTGGGTTGACGACTGACGTTTT
A S L Q C Y N C P N P T A D C K>

TRANSLATION OF HUCCBAM/RIMP [A] >

560 570 580 590 600
CAGCCGTCAATTGTTTCATCTGATTTTGATGCGTGTCTCATTACCAAAGCT
GTCGGCAGTTAACAAGTAGACTAAACTACGCACAGAGTAATGGTTTCGA
T A V N C S S D F D A C L I T K A>

TRANSLATION OF HUCCBAM/RIMP [A] >

610 620 630 640 650
GGGTTACAAGTGATAACAAGTGTTGGAAGTTTGAGCATTGCAATTTCAA
CCCAATGTTTCACATATTGTTTCACAACCTTCAAACCTCGTAACGTAAAGTT
G L Q V Y N K C W K F E H C N F N>

TRANSLATION OF HUCCBAM/RIMP [A] >

660 670 680 690 700
CGACGTCACAACCCGCTTGAGGGAAAATGAGCTAACGTACTACTGCTGCA
GCTGCAGTGTTGGGCGAACTCCCTTTTACTCGATTGCATGATGACGACGT
D V T T R L R E N E L T Y Y C C>

TRANSLATION OF HUCCBAM/RIMP [A] >

710 720 730 740 750
AGAAGGACCTGTGTAACCTTAAACGAACAGCTTGAAAATGGTGGGACATCC
TCTTCCTGGACACATTGAAATTGCTTGTGCGAACTTTTACCACCCTGTAGG
K K D L C N F N E Q L E N G G T S>

TRANSLATION OF HUCCBAM/RIMP [A] >

760 770 780 790 800
TTATCAGAGAAAACAGTTCTTCTGCTGGTGACTCCATTTCTGGCAGCAGC

AATAGTCTCTTTTGTCAAGAAGACGACCACTGAGGTAAAGACCGTCGTCG
L S E K T V L L L V T P F L A A A>
_____TRANSLATION OF HUCCBAM/RIMP [A] _____>

810 820 830
CTGGAGCCTTCATCCCTAAGTCGGAATTCC
GACCTCGGAAGTAGGGATTCAGCCTTAAGG
W S L H P *>
_____TRANSLATION _____>

Sequence Range: 1 to 261

10 20 30 40 50
MGIQGGSVLFGLLLVLAVFCHSGHSLQMHVAQPAVVLAASSRGIASFVCEY
60 70 80 90 100
ASPGKATEVRVTVLRQADSQVTEVCAATYMTGNELTFLDDSICTGTSSGN
110 120 130 140 150
QVNLTIQGLRAMDTGLYICKVELMYPPPYLGIGNGTQIYVIDPEPCPDS
160 170 180 190 200
DASASASLQCYNCPNPTADCKTAVNCSSDFDAKLTKAGLQVYNKCWFFE
210 220 230 240 250
HCNFNDVTTRLRENELTYCCKKDLCNFNEQLENGGSLSSEKTVLLLVTP
260
FLAAAWSLHP*

Fig 2B2

Sequence Range: 1 to 672

```

      10      20      30      40      50
ATGGCTCGTTTCGGATTCCGGAGCCATGGGGCTTGGCTGGAGCTTACTTC
TACCGAGCAAAGCCTAAGGCCTCGGTACCCCGAACCGACCTCGAATGAAG
  M  A  R  F  G  F  R  S  H  G  A  W  L  E  L  T  S >
      _____TRANSLATION OF PCTLA4SEQ [ A] _____>

      60      70      80      90     100
TAGGACCTGGCCCTGTACAGCTCTGTTTTCTTCTTCTTCATCCCTGTCT
ATCCTGGACCGGGACATGTCTGAGACAAAAGAGAAGAGAAGTAGGGACAGA
  R  T  W  P  C  T  A  L  F  S  L  L  F  I  P  V >
      _____TRANSLATION OF PCTLA4SEQ [ A] _____>

     110     120     130     140     150
TCTCCAAAGGGATGCACGTGGCCCAGCCTGCAGTGGTGCTGGCCAACAGC
AGAGGTTTCCCTACGTGCACCGGGTCGGACGTCACCACGACCGGTTGTCG
  F  S  K  G  M  H  V  A  Q  P  A  V  V  L  A  N  S >
      _____TRANSLATION OF PCTLA4SEQ [ A] _____>

     160     170     180     190     200
CGGGGTGTTGCCAGCTTTGTGTGTGAGTATGGGTCTGCAGGCAAAGCTGC
GCCCCACAACGGTTCGAAACACACACTCATACCCAGACGTCGGTTTCGACG
  R  G  V  A  S  F  V  C  E  Y  G  S  A  G  K  A  A >
      _____TRANSLATION OF PCTLA4SEQ [ A] _____>

     210     220     230     240     250
CGAGGTCCGGGTGACAGTGCTGCGGCGGGCCGGCAGCCAGATGACTGAAG
GCTCCAGGCCCACTGTACGACGCCGCCCGGCCGTCGGTCTACTGACTTC
  E  V  R  V  T  V  L  R  R  A  G  S  Q  M  T  E >
      _____TRANSLATION OF PCTLA4SEQ [ A] _____>

     260     270     280     290     300
TCTGTGCCGCGACATATACTGTGGAGGATGAGTTGACCTTCCTTGATGAC
AGACACGGCGCTGTATATGACACCTCCTACTCAACTGGAAGGAAGTACTG
  V  C  A  A  T  Y  T  V  E  D  E  L  T  F  L  D  D >
      _____TRANSLATION OF PCTLA4SEQ [ A] _____>

     310     320     330     340     350
TCTACATGCACTGGCACCTCCACCGAAAACAAAGTGAACCTCACCATCCA
AGATGTACGTGACCGTGGAGGTGGCTTTTGTTCCTTGGAGTGGTAGGT
  S  T  C  T  G  T  S  T  E  N  K  V  N  L  T  I  Q >
      _____TRANSLATION OF PCTLA4SEQ [ A] _____>

     360     370     380     390     400
AGGGCTGAGAGCCGTGGACACTGGGCTCTACATCTGCAAGGTGGAGCTCC
TCCCGACTCTCGGCACCTGTGACCCGAGATGTAGACGTTCCACCTCGAGG

```

Fig 2c1

G L R A V D T G L Y I C K V E L>

TRANSLATION OF PCTLA4SEQ [A] _____>

410 420 430 440 450
TGTACCCACCACCCTACTATGTGGGTATGGGCAACGGGACCCAGATTTAT
ACATGGGTGGTGGGATGATACACCCATAACCGTTGCCCTGGGTCTAAATA
L Y P P P Y Y V G M G N G T Q I Y>

TRANSLATION OF PCTLA4SEQ [A] _____>

460 470 480 490 500
GTCATTGATCCAGAACCATGCCCAGATTCTGATTTCTGCTCTGGATCCT
CAGTAACTAGGTCTTGGTACGGGTCTAAGACTAAAGGACGAGACCTAGGA
V I D P E P C P D S D F L L W I L>

TRANSLATION OF PCTLA4SEQ [A] _____>

510 520 530 540 550
GGCAACAGTTAGTTCAGGGTTGTTTTTTTACAGCTTCCTCATCACAGCTG
CCGTTGTCAATCAAGTCCCAACAAAAAATGTCGAAGGAGTAGTGTCGAC
A T V S S G L F F Y S F L I T A>

TRANSLATION OF PCTLA4SEQ [A] _____>

560 570 580 590 600
TTTCTTTGAGCAAAATGCTAAAGAAAAGAAGTCCTCTTACTACAGGGGTC
AAAGAACTCGTTTTACGATTTCTTTTCTTCAGGAGAATGATGTCCCCAG
V S L S K M L K K R S P L T T G V>

TRANSLATION OF PCTLA4SEQ [A] _____>

610 620 630 640 650
TATGTGAAAAATGCCCCGACAGAGCCAGAATGTGAAAAGCAATTTTCAGCC
ATACACTTTTTACGGGGCTGTCTCGGTCTTACACTTTTCGTTAAAGTCGG
Y V K N A P T E P E C E K Q F Q P>

TRANSLATION OF PCTLA4SEQ [A] _____>

660 670
TTATTTTATTCCCATCAACTGA
AATAAAATAAGGGTAGTTGACT
Y F I P I N *>

TRANSLATION OF _____>

Sequence Range: 1 to 224

```

      10      20      30      40      50
MACLG FQRHKAQLNLAARTWPCTLLFELLFIPVFECKAMHVAQPAVV LASS

      60      70      80      90     100
RGIASFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMTGNELTFLDD

     110     120     130     140     150
SICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPPPYLGI GNGTQIY

     160     170     180     190     200
VIDPEPCPDSDFLWILAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTTGV

     210     220
YVKMPPTPEPECEKQFQPYFIPIN*
```

Fig 2c2 2D2

Sequence Range: 1 to 672

```

      10      20      30      40      50
ATGGCTTGCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCTGC
TACCGAACGGAACCTAAAGTCGCCGTGTTCCGAGTCGACTTGGACCGACG
  M  A  C  L  G  F  Q  R  H  K  A  Q  L  N  L  A  A>
_____TRANSLATION OF HCTLA4SEQ [ A] _____>

      60      70      80      90     100
CAGGACCTGGCCCTGCACTCTCCTGTTTTTCTTCTCTTCATCCCTGTCT
GTCCTGGACCGGGACGTGAGAGGACAAAAAGAAGAGAAGTAGGGACAGA
  R  T  W  P  C  T  L  L  F  F  L  L  F  I  P  V>
_____TRANSLATION OF HCTLA4SEQ [ A] _____>

     110     120     130     140     150
TCTGCAAAGCAATGCACGTGGCCCAGCCTGCTGTGGTACTGGCCAGCAGC
AGACGTTTCGTTACGTGCACCGGGTCGGACGACACCATGACCGGTCGTCG
  F  C  K  A  M  H  V  A  Q  P  A  V  V  L  A  S  S>
_____TRANSLATION OF HCTLA4SEQ [ A] _____>

     160     170     180     190     200
CGAGGCATCGCCAGCTTTGTGTGTGAGTATGCATCTCCAGGCAAAGCCAC
GCTCCGTAGCGGTCGAAACACACACTCATACTAGAGGTCCGTTTCGGTG
  R  G  I  A  S  F  V  C  E  Y  A  S  P  G  K  A  T>
_____TRANSLATION OF HCTLA4SEQ [ A] _____>

     210     220     230     240     250
TGAGGTCCGGGTGACAGTGCTTCGGCAGGCTGACAGCCAGGTGACTGAAG
ACTCCAGGCCCACTGTCACGAAGCCGTCCGACTGTCGGTCCACTGACTTC
  E  V  R  V  T  V  L  R  Q  A  D  S  Q  V  T  E>
_____TRANSLATION OF HCTLA4SEQ [ A] _____>

     260     270     280     290     300
TCTGTGCGGCAACCTACATGACGGGGAATGAGTTGACCTTCCTAGATGAT
AGACACGCCGTTGGATGTACTGCCCTTACTCAACTGGAAGGATCTACTA
  V  C  A  A  T  Y  M  T  G  N  E  L  T  F  L  D  D>
_____TRANSLATION OF HCTLA4SEQ [ A] _____>

     310     320     330     340     350
TCCATCTGCACGGGCACCTCCAGTGGAATCAAGTGAACCTCACTATCCA
AGGTAGACGTGCCCGTGGAGGTCACCTTTAGTTCACTTGGAGTGATAGGT
  S  I  C  T  G  T  S  S  G  N  Q  V  N  L  T  I  Q>
_____TRANSLATION OF HCTLA4SEQ [ A] _____>

     360     370     380     390     400
AGGACTGAGGGCCATGGACACGGGACTCTACATCTGCAAGGTGGAGCTCA
TCCTGACTCCCGGTACCTGTGCCCTGAGATGTAGACGTTCCACCTCGAGT
```

Fig 2D1

G L R A M D T G L Y I C K V E L>

TRANSLATION OF HCTLA4SEQ [A] >

410 420 430 440 450
TGTACCCACCGCCATACTACCTGGGCATAGGCAACGGAACCCAGATTTAT
ACATGGGTGGCGGTATGATGGACCCGTATCCGTTGCCTTGGGTCTAAATA
M Y P P P Y Y L G I G N G T Q I Y>

TRANSLATION OF HCTLA4SEQ [A] >

460 470 480 490 500
GTAATTGATCCAGAACCGTGCCAGATTCTGACTTCCTCCTCTGGATCCT
CATTAACTAGGTCTTGGCACGGGTCTAAGACTGAAGGAGGAGACCTAGGA
V I D P E P C P D S D F L L W I L>

TRANSLATION OF HCTLA4SEQ [A] >

510 520 530 540 550
TGCAGCAGTTAGTTCGGGGTTGTTTTTTTATAGCTTCTCCTCACAGCTG
ACGTCGTCAATCAAGCCCCAACAAAAAATATCGAAAGAGGAGTGTCGAC
A A V S S G L F F Y S F L L T A>

TRANSLATION OF HCTLA4SEQ [A] >

560 570 580 590 600
TTTCTTTTGAGCAAAATGCTAAAGAAAAGAAGCCCTCTTACAACAGGGGTC
AAAGAAACTCGTTTTACGATTTCTTTTCTTCGGGAGAATGTTGTCCCCAG
V S L S K M L K K R S P L T T G V>

TRANSLATION OF HCTLA4SEQ [A] >

610 620 630 640 650
TATGTGAAAATGCCCCAACAGAGCCAGAATGTGAAAAGCAATTTTCAGCC
ATACACTTTTACGGGGGTTGTCTCGGTCTTACACTTTTCGTTAAAGTCGG
Y V K M P P T E P E C E K Q F Q P>

TRANSLATION OF HCTLA4SEQ [A] >

660 670
TTATTTTATTCCCATCAATTGA
AATAAAATAAGGGTAGTTAACT
Y F I P I N *>

TRANSLATION OF >

Sequence Range: 1 to 224

```

      10      20      30      40      50
MARFGFRSHGAWLELTSRTWPCTALFSLLEFIPVFSKGMHVAQPAVVLANS

      60      70      80      90     100
RGVASFVCEYGSAGKAAEVRVTVLRRAGSQMTEVCAATYTVEDELTFLLDD

     110     120     130     140     150
STCTGTSTENKVNLTIQGLRAVDTLGLYICKVELLYPPPYVGMNGTQII

     160     170     180     190     200
VIDPEPCPDSDFLWILATVSSGLFFYSFLITAVSLSKMLKKRSPLTTGV

     210     220
YVKNAPEPECEKQFPYFIPIN*
```

~~202~~ → 202

Sequence Range: 1 to 476

```

      10      20      30      40      50
GAATTCGGGGGCTGAGCGCAGAAGCGGCTCGAGGCTGGAAGAGGATCCT
CTTAAGGCCCGGACTCGCGTCTTCGCCGAGCTCCGACCTTCTCCTAGGA

      60      70      80      90     100
GGGCGCCGCAGGTTCTGTGGACAATCACAATGGGAATCCAAGGAGGGTCT
CCCGCGGCGTCCAAGACACCTGTTAGTGTTACCCTTAGGTTCCCTCCCAGA
      M G I Q G G S>
      _____TRANSLATION OF _____>

     110     120     130     140     150
GTCCTGTTCTGGGCTGCTGCTCGTCCTGGCTGTCTTCTGCCATTCAGGTCA
CAGGACAAGCCCGACGACGAGCAGGACCGACAGAAGACGGTAAGTCCAGT
  V L F G L L L V L A V F C H S G H>
  _____TRANSLATION OF HCD59SEQ [ A ] _____>

     160     170     180     190     200
TAGCCTGCAGTGCTACAACCTGTCCTAACCCAACTGCTGACTGCAAAACAG
ATCGGACGTCACGATGTTGACAGGATTGGGTTGACGACTGACGTTTTTGTC
  S L Q C Y N C P N P T A D C K T>
  _____TRANSLATION OF HCD59SEQ [ A ] _____>

     210     220     230     240     250
CCGTCAATTGTTTCATCTGATTTTGATGCGTGTCTCATTACCAAAGCTGGG
GGCAGTTAACAAGTAGACTAAACTACGCACAGAGTAATGGTTTTCGACCC
A V N C S S D F D A C L I T K A G>
  _____TRANSLATION OF HCD59SEQ [ A ] _____>

     260     270     280     290     300
TTACAAGTGTATAACAAGTGTTGGAAGTTTGAGCATTGCAATTTCAACGA
AATGTTACATATTGTTTACAACCTTCAAACCTCGTAACGTTAAAGTTGCT
  L Q V Y N K C W K F E H C N F N D>
  _____TRANSLATION OF HCD59SEQ [ A ] _____>

     310     320     330     340     350
CGTCACAACCCGCTTGAGGGAAAATGAGCTAACGTACTACTGCTGCAAGA
GCAGTGTTGGGCGAACTCCCTTTTACTCGATTGCATGATGACGACGTTCT
  V T T R L R E N E L T Y Y C C K>
  _____TRANSLATION OF HCD59SEQ [ A ] _____>

     360     370     380     390     400
AGGACCTGTGTAACCTTTAACGAACAGCTTGAAAATGGTGGGACATCCTTA
TCCTGGACACATTGAAATTGCTTGTCGAACTTTTACCACCCTGTAGGAAT
K D L C N F N E Q L E N G G T S L>
  _____TRANSLATION OF HCD59SEQ [ A ] _____>

```

Fig 2E1

410 420 430 440 450
TCAGAGAAAACAGTTCTTCTGCTGGTGACTCCATTTCTGGCAGCAGCCTG
AGTCTCTTTTGTCAAGAAGACGACCACTGAGGTAAAGACCGTCGTCGGAC
S E K T V L L L V T P F L A A A W>
_____TRANSLATION OF HCD59SEQ [A] _____>

460 470
GAGCCTTCATCCCTAAGTCGGAATTC
CTCGGAAGTAGGGATTTCAGCCTTAAG
S L H P *>
____TRANSLATI____>

Sequence Range: 1 to 129

10	20	30	40	50
MGIQGGSVLFGLLLVLA V FCHSGHSLQCYNC PNPTADCKTAVNCSSDFDA				
60	70	80	90	100
CLITKAGLQVYNKCWKFEHCNFNDVTTTRLRENELTYYCCKKDL CNFNEQL				
110	120			
ENGGTSLSEKTVLLLVT PFLAAAWSLHP*				

2E2

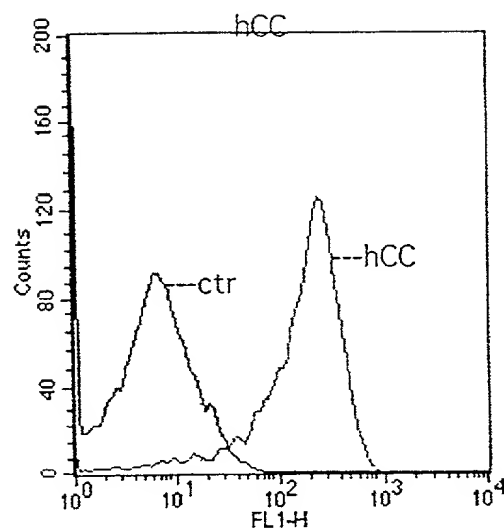
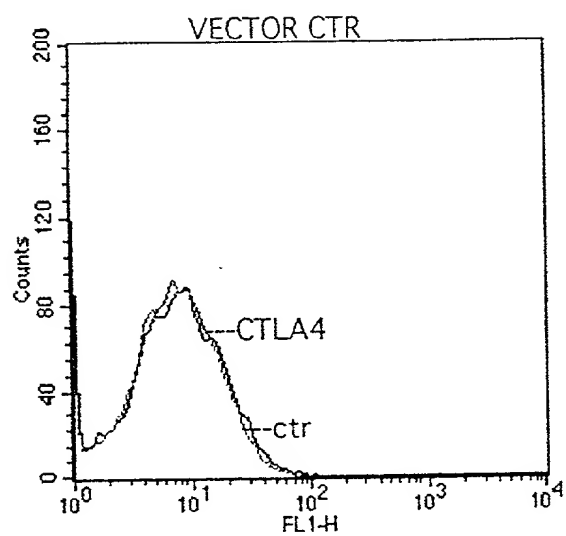


Fig 3

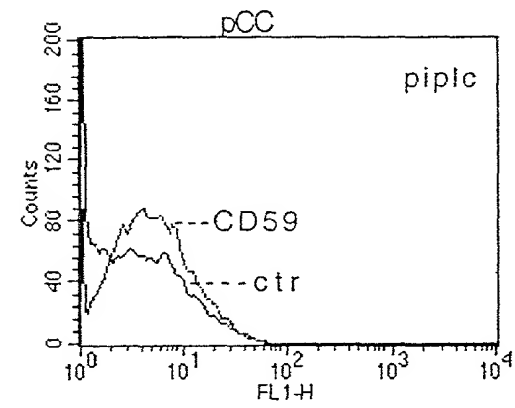
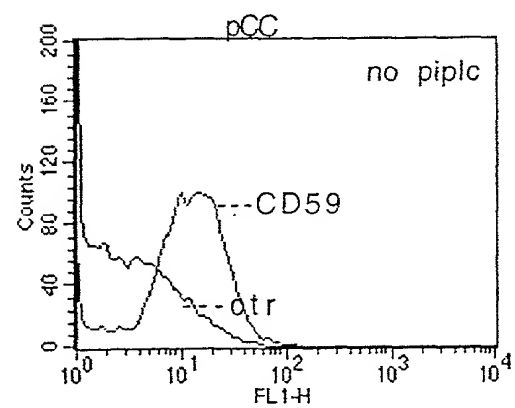
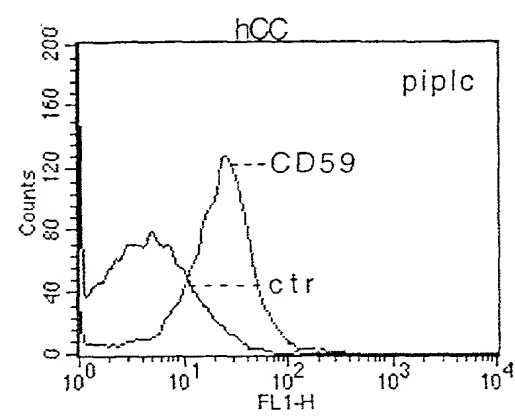
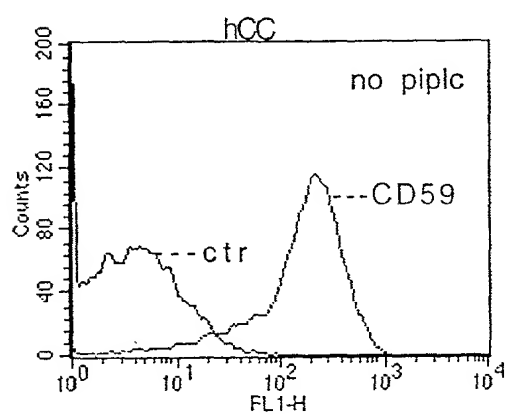
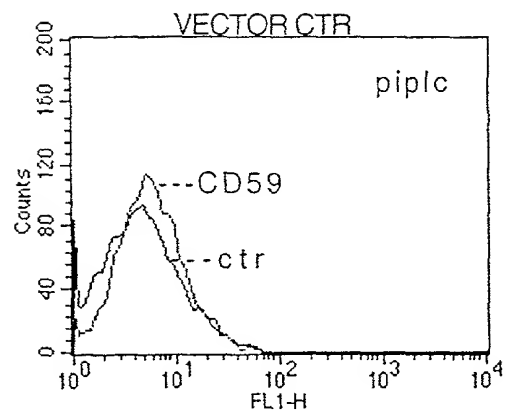
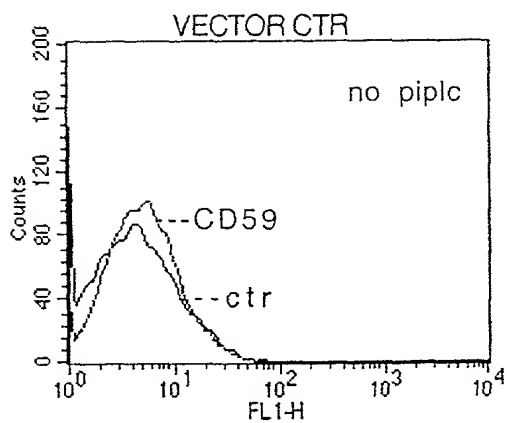


Fig 4

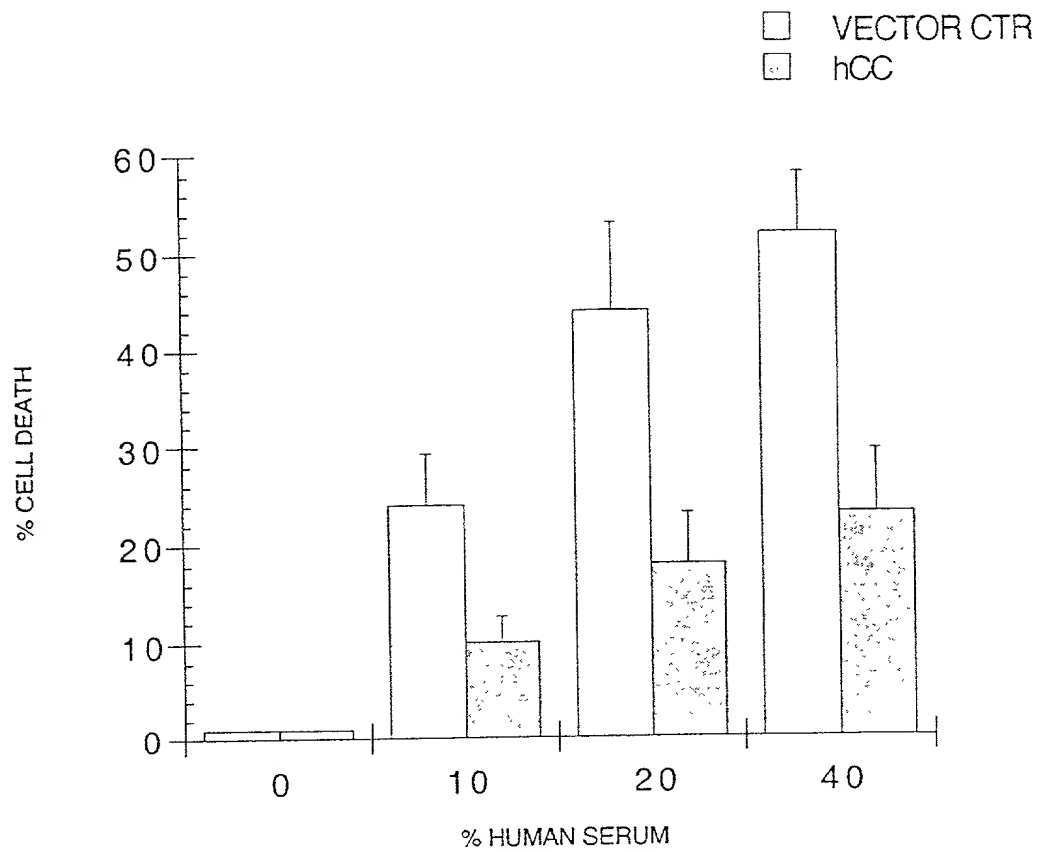


Fig 5

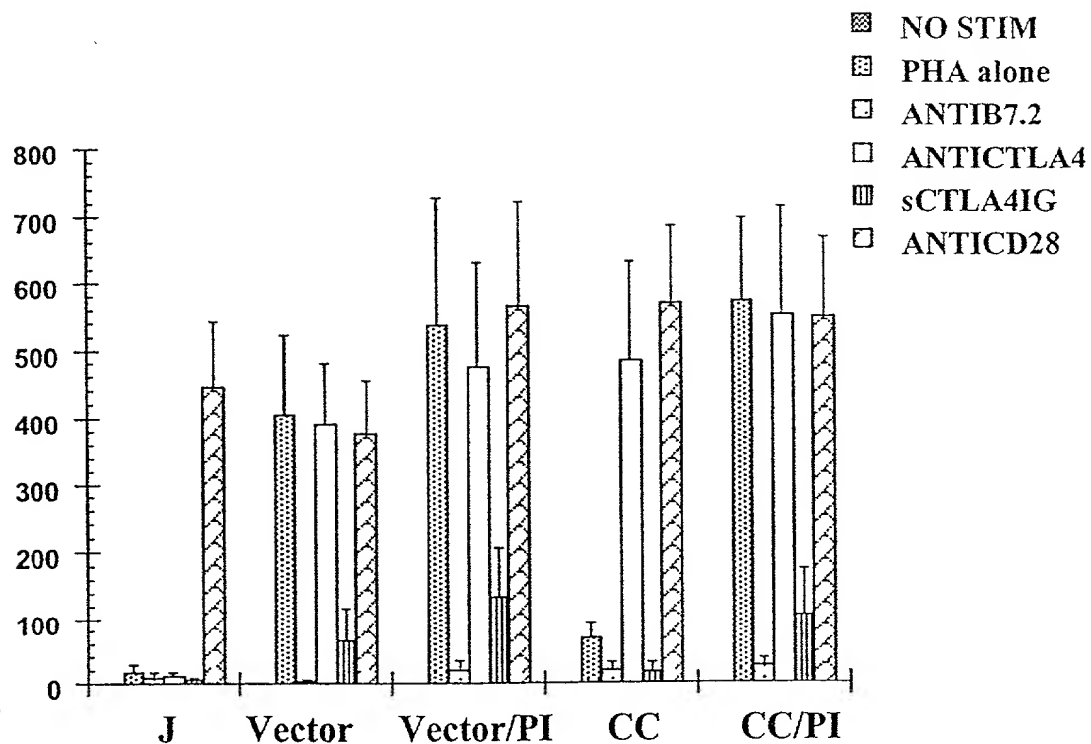


Figure 6 Co-Culture of Jurkat cells with Vector control PAECs or with CC PAECs with and without PI-PLC treatment.

Sequence Range: 1 to 314

10 20 30 40 50
MTVARPSVPAALPLLGLPRLLLLVLLCLPAVWGDCGLPPDVPNQERLE
60 70 80 90 100
GRTSFPEDTVITYKCEESFVKIPGEKDSVICKLGSQWSDIEEFCNPSCET
110 120 130 140 150
PTRLNSASLKQPYITQNYFPVGTVEYECRPGYRREPSLSPKLTCLDLE
160 170 180 190 200
WSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGKLEFCT
210 220 230 240 250
SSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQGERDHYGYPCCVT
260 270 280 290 300
YACNKGFTMIGEHSIYCTVNNDGEWSGPPPECRGKSLTSKVPPTVQKPT
310
TVNVPTTEVSPTSQ

QNLK ✓

FAST ✓

FAST ✓

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314